

SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT, K+betaM3

<130> D0114.np

<150> US 60/267,039

<151> 2001-02-05

<150> US 60/281,224

<151> 2001-04-03

<160> 76

<170> PatentIn version 3.0

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cggcgcacct gctgccccga acccctggct ccagggggca atgagggggc agtgggaaggg    300
gcactactcc tggggcattg cctagagaag cgagaccgtc ccgccctccc gctggccctc     360
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Gly Thr Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala His Val His
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His Thr Asp Val Gly Ser His Met Tyr Thr Ser Ser Leu Ala Thr Leu
 35 40 45

Thr Lys Tyr Pro Val Ser Arg Ile Arg Arg Leu Cys Asp Gly Thr Glu
 50 55 60

Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Thr Asp Arg Asp
 65 70 75 80

Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu
 85 90 95

Leu Ile Leu Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala
 100 105 110

Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys
 115 120 125

Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val
 130 135 140

Cys Val Ala Pro Asp Leu Arg Glu Arg Ile Thr Leu Ser Gly Asp Lys
 145 150 155 160

Ser Leu Val Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys Asn
 165 170 175

Phe Ile Ser Ala Gly Trp Asn His Asp Ser Thr His Ile Val Arg Phe
 180 185 190

Pro Leu Ser Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu Arg
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Gly Ser Ser
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His Ile Asp Val Gly Gly His Met Tyr Thr Ser Ser Leu Ala Thr Leu
 35 40 45

Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg Leu Phe Asp Gly Thr Glu
 50 55 60

Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp
 65 70 75 80

Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu
 85 90 95

Leu Ile Pro Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala
 100 105 110

Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys
 115 120 125

Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val
 130 135 140

Val Arg Val Ala Pro Asp Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp
 145 150 155 160

Lys Ser Leu Ile Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys
 165 170 175

Asn Ser Val Asn Ala Gly Trp Asn His Asp Ser Thr His Val Ile Arg
 180 185 190

Phe Pro Leu Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu
 195 200 205

Arg Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly Gly
 210 215 220

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 35 40 45

Pro Thr Pro Pro Ala Ser Ser Ser Val Thr Pro Leu Gly Leu Pro Gly
 50 55 60

Ala Val Ala Ala Ala Ala Ala Ala Val Gly Gly Ala Ser Ser Ala Gly
 65 70 75 80

Ala Ser Ser Tyr Leu His Gly Asn His Lys Pro Ile Thr Gly Ile Pro
 85 90 95

Cys Val Ala Ala Ala Ser Arg Tyr Thr Ala Pro Val His Ile Asp Val
 100 105 110

Gly Gly Thr Ile Tyr Thr Ser Ser Leu Glu Thr Leu Thr Lys Tyr Pro
 115 120 125

Glu Ser Lys Leu Ala Lys Leu Phe Asn Gly Gln Ile Pro Ile Val Leu
 130 135 140

Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp Gly Gly Met Phe
 145 150 155 160

Arg His Ile Leu Asn Phe Met Arg Asn Ser Arg Leu Leu Ile Ala Glu
 165 170 175

Asp Phe Pro Asp Leu Glu Leu Leu Leu Glu Glu Ala Arg Tyr Tyr Glu
 180 185 190

Val Glu Pro Met Ile Lys Gln Leu Glu Ser Met Arg Lys Asp Arg Val

195 200 205

Arg Asn Gly Asn Tyr Leu Val Ala Pro Pro Thr Pro Pro Ala Arg His
 210 215 220

Ile Lys Thr Ser Pro Arg Thr Ser Ala Ser Pro Glu Cys Asn Tyr Glu
 225 230 235 240

Val Val Ala Leu His Ile Ser Pro Asp Leu Gly Glu Arg Ile Met Leu
 245 250 255

Ser Ala Glu Arg Ala Leu Leu Asp Glu Leu Phe Pro Glu Ala Ser Gln
 260 265 270

Ala Thr Gln Ser Ser Arg Ser Gly Val Ser Trp Asn Gln Gly Asp Trp
 275 280 285

Gly Gln Ile Ile Arg Phe Pro Leu Asn Gly Tyr Cys Lys Leu Asn Ser
 290 295 300

Val Gln Val Leu Thr Arg Leu Leu Asn Ala Gly Phe Thr Ile Glu Ala
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Ser Val Gly Gly Gln Gln Phe Ser Glu Tyr Leu Leu Ala Arg Arg Val
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tatatcttga atttttotacg aacatccaaa ctctcattc ttgatgattt caaggactac 180

actttgttat atgaagaggc aaaatatttt cagcttcagc ccatgtgttg gagatggaaa 240

gatggaagca ggacagagaa actggtcgct tttcaaggcc ctgtgagtgc cttgttgttt 300

gtgtggcccc agacctcaga gaaaggatca cgctaagtgg tgacaaatcc ttggtagaag 360

aagtgtttcc agagatcggc gatgtgatgt gcaactttat cagtgcaggc tggaatcacg 420

actccacgca catcgtcagg tttccactaa gtggctactg tcacctcaac tcagtccagg 480

tcctcgagag gttgcagcaa agaggatttg aaatcgtagg ctctgtagg ggaggagtgg 540

gcttgtccta gttcagcaaa tacgtccttc atagggaact gaggcggatg ccttcccgtg 600

ccctccatca tctggataaa gcaagagcct ctggactaaa cggacatatt tcttatgcaa 660

aaaggaaaac acacacaact aataaacaaa taataaaaaa gggacatttg tgtgcagttg 720
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 35 40 45
 Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu
 50 55 60
 Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro
 65 70 75 80
 Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr
 85 90 95
 Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr
 100 105 110
 Pro Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys
 115 120 125
 Leu Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr
 130 135 140
 Ile Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe
 145 150 155 160
 Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser
 165 170 175
 Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val
 180 185 190
 His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr
 195 200 205
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 1 5 10

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Phe Glu Ile Val Gly Ser Cys Arg Gly Gly Val Gly Ser
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Gly Thr Glu Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Thr
35 40 45

Asp Arg Asp Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr
50 55 60

Ser Lys Leu Leu Ile Leu Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr
65 70 75 80

Glu Glu Ala Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu
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20 25 30
Thr Ile Gly Thr Leu Thr Lys Asn Asn Asp Thr Met Leu Ser Ala Met
35 40 45
Phe Ser Gly Arg Met Glu Val Leu Thr Asp Ser Glu Gly Trp Ile Leu
50 55 60
Ile Asp Arg Cys Gly Asn His Phe Gly Ile Ile Leu Asn Tyr Leu Arg
65 70 75 80
Asp Gly Thr Val Pro Leu Pro Glu Thr Asn Lys Glu Ile Ala Glu Leu
85 90 95
Leu Ala Glu Ala Lys Tyr Tyr Cys Ile Thr Glu Leu Ala Ile Ser Cys
100 105 110
Glu Arg Ala Leu Tyr Ala His Gln Glu Pro Lys Pro Ile Cys Arg Ile
115 120 125
Pro Leu Ile Thr Ser Gln Lys Glu Glu Gln Leu Leu Leu Ser Val Ser
130 135 140
Leu Lys Pro Ala Val Ile Leu Val Val Gln Arg Gln Asn Asn Lys Tyr
145 150 155 160
Ser Tyr Thr Ser Thr Ser Asp Asp Asn Leu Leu Lys Asn Ile Glu Leu
165 170 175
Phe Asp Lys Leu Ser Leu Arg Phe Asn Glu Arg Ile Leu Phe Ile Lys
180 185 190

Asp Val Ile Gly Pro Ser Glu Ile Cys Cys Trp Ser Phe Tyr Gly His
 195 200 205
 Gly Lys Lys Val Ala Glu Val Cys Cys Thr Ser Ile Val Tyr Ala Thr
 210 215 220
 Asp Arg Lys His Thr Lys Val Glu Phe Pro Glu Ala Arg Ile Tyr Glu
 225 230 235 240
 Glu Thr Leu Gln Val Leu Leu Tyr Glu Asn Arg Asn Ala Pro Asp Gln
 245 250 255
 Glu Leu Met Gln Ala Thr Ser Ser Ala Arg Val Gly Ser Ala Ser Gly
 260 265 270
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tcctatgtgc tgactcagcc acc

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tcttctgagc tgactcagga ccc

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35 40 45
Gln Glu Ser Lys Cys His Leu Ile Glu Thr Asn Ile Arg Asp Gln Glu
50 55 60
Glu Leu Lys Gly Lys Lys Val Pro Gln Tyr Pro Cys Leu Trp Val Asn
65 70 75 80
Val Ser Ala Ala Gly Arg Trp Ala Val Leu Tyr His Thr Glu Asp Thr
85 90 95
Arg Asp Gln Asn Gln Gln Cys Ser Tyr Ile Pro Gly Ser Val Asp Asn
100 105 110
Tyr Gln Thr Ala Arg Ala Asp Val Glu Lys Val Arg Ala Lys Phe Gln
115 120 125
Glu Gln Gln Val Phe Tyr Cys Phe Ser Ala Pro Arg Gly Asn Glu Thr
130 135 140
Ser Val Leu Phe Gln Arg Leu Tyr Gly Pro Gln Ala Leu Leu Phe Ser
145 150 155 160
Leu Phe Trp Pro Thr Phe Leu Leu Thr Gly Gly Leu Leu Ile Ile Ala
165 170 175
Met Val Lys Ser Asn Gln Tyr Leu Ser Ile Leu Ala Ala Gln Lys
180 185 190